

GEPHE SUMMARY

SCN8A (Nav1.6) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> )	Gephebase Gene	GP00001655	GepheID
Gephebase="SCN8A (Nav1.6)"#gephebase-summary-title)			Main curator
Published	Entry Status	Prigent	

PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> )	Trait Category		
Category="Physiology"#gephebase-summary-title)			
Xenobiotic resistance (TTX) ( <a (ttx)"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=" resistance="" xenobiotic="">https://www.gephebase.org/search-criteria?/and+Trait="Xenobiotic resistance (TTX)"#gephebase-summary-title</a> )	Trait		
	Trait State in Taxon A		
TTX-Sensitive Erythrolamprus (=Liophis) poecilogyrus			
	Trait State in Taxon B		
TTX-Resistant Erythrolamprus (=Liophis) epinephelus			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Interspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> )			
Status="Interspecific"#gephebase-summary-title)			
	Taxon A	Taxon B	
	Latin Name		Latin Name
Erythrolamprus poecilogyrus		Erythrolamprus epinephelus	
( <a erythrolamprus="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=" poecilogyrus"#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Erythrolamprus poecilogyrus"#gephebase-summary-title</a> )		( <a epinephelus"#gephebase-summary-title"="" erythrolamprus="" href="https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Erythrolamprus epinephelus"#gephebase-summary-title</a> )	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
Coluber poecilogyrus; Liophis poecilogyrus; Coluber poecilogyrus Wied-Neuwied, 1825; Liophis poecilogyrus (Wied-Neuwied, 1825); AMNH 3594; AMNH:3594		Erythrolamprus epinephelus; Leimadophis epinephelus; Liophis epinephelus; Liophis epinephelus Cope, 1862; ANSP 3688; ANSP:3688	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Serpentes; Colubroidea; Dipsadidae; Erythrolamprus		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata; Toxicofera; Serpentes; Colubroidea; Dipsadidae; Erythrolamprus	
	Parent		Parent
Erythrolamprus () - (Rank: genus)		Erythrolamprus () - (Rank: genus)	
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 121327">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 121327</a> )		( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 121327">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 121327</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
338838		758879	
( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 338838">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 338838</a> )		( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 758879">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 758879</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

SCN8A	Generic Gene Name	UniProtKB Erythrolamprus epinephelus
	Synonyms	A0A1B0Z7B3 ( <a href="http://www.uniprot.org/uniprot/A0A1B0Z7B3">http://www.uniprot.org/uniprot/A0A1B0Z7B3</a> )
-		GenebankID or UniProtKB
	String	0
	Sequence Similarities	
Belongs to the sodium channel (TC 1.A.1.10) family.		
	GO - Molecular Function	
GO:0005244 : voltage-gated ion channel activity		
( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005244">https://www.ebi.ac.uk/QuickGO/term/GO:0005244</a> )		
GO:0005248 : voltage-gated sodium channel activity		
( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005248">https://www.ebi.ac.uk/QuickGO/term/GO:0005248</a> )		
	GO - Biological Process	
GO:0034765 : regulation of ion transmembrane transport		
( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0034765">https://www.ebi.ac.uk/QuickGO/term/GO:0034765</a> )		

GO:0001518 : voltage-gated sodium channel complex  
 (https://www.ebi.ac.uk/QuickGO/term/GO:0001518)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
G1717M in DIV domain (not tested)	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Historical Contingency in a Multigene Family Facilitates Adaptive Evolution of Toxin Resistance. (2016) (https://pubmed.ncbi.nlm.nih.gov/27291053)

McGlothlin JW; Kobiela ME; Feldman CR; Castoe TA; Geffney SL; Hanifin CT; Toledo G; Vonk FJ; Richardson MK; Brodie ED; Pfreder ME; Brodie ED

Novel adaptations must originate and function within an already established genome [1]. As a result, the ability of a species to adapt to new environmental challenges is predicted to be highly contingent on the evolutionary history of its lineage [2-6]. Despite a growing appreciation of the importance of historical contingency in the adaptive evolution of single proteins [7-11], we know surprisingly little about its role in shaping complex adaptations that require evolutionary change in multiple genes. One such adaptation, extreme resistance to tetrodotoxin (TTX), has arisen in several species of snakes through coevolutionary arms races with toxic amphibian prey, which select for TTX-resistant voltage-gated sodium channels (Nav) [12-16]. Here, we show that the relatively recent origins of extreme toxin resistance, which involve the skeletal muscle channel Nav1.4, were facilitated by ancient evolutionary changes in two other members of the same gene family. A substitution conferring TTX resistance to Nav1.7, a channel found in small peripheral neurons, arose in lizards  $\sim$ 4170 million years ago (mya) and was present in the common ancestor of all snakes. A second channel found in larger myelinated neurons, Nav1.6, subsequently evolved resistance in four different snake lineages beginning  $\sim$ 438 mya. Extreme TTX resistance has evolved at least five times within the past 12 million years via changes in Nav1.4, but only within lineages that previously evolved resistant Nav1.6 and Nav1.7. Our results show that adaptive protein evolution may be contingent upon enabling substitutions elsewhere in the genome, in this case, in paralogs of the same gene family.

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Additional References

RELATED GEPHE

1 (SCN4A (Nav1.4)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^338838^/and+Trait=Xenobiotic resistance/or+Taxon ID=^758879^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation